

Model for Camel IgG 3

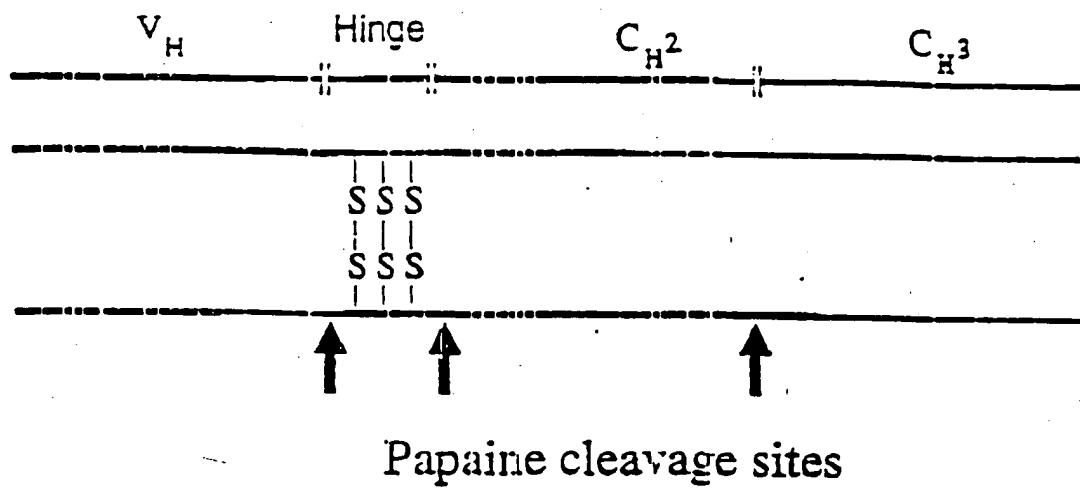


Fig 5: Schematic representation of Camel IgG₃ model.

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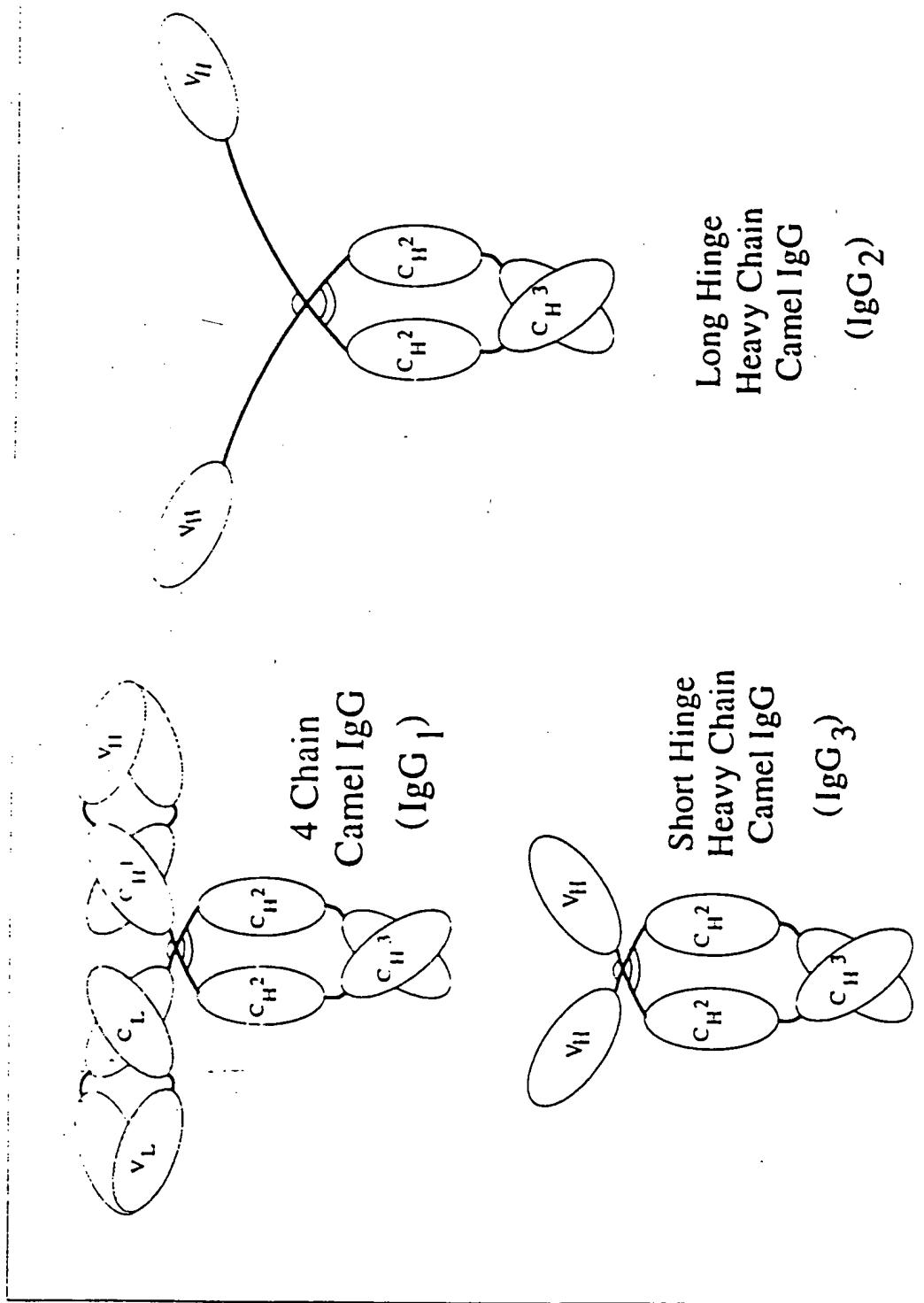


Fig 6: A schematic representation of Camel immunoglobulins IgG₁, the putative IgG₂ and IgG₃. The large (Pro-X)₁₂ of the putative IgG₂molecule can be modelled into a 6 aa repeat

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DR01006	C-----	TCGAG---TCTGGGGGAGG
DR27006	C-----	TCGAG---TCTGGGGGAGG
DR03006	C-----AGGTGA-----	AACTGCTCGAG---TCTGGAGGGAGG
DR11006	C-----	TCGAG---TCTGGGGGAGG
DR24006	C-----AGGTGA-----	AACTGCTCGAG---TCTGGGGGAGG
DR16006	C-----	TCGAG---TCTGGAGGGAGG
DR19006	C-----	TCGAG---TCTGGAGGGAGG
DR07006	C-----	TCGAG---TCTGGGGGAGG
DR16006	C-----	TCGAG---TCTGGGGGAGG
DR20006	C-----	TCGAG---TCAGGGGGAGG
DR25006	C-----	TCGAG---TCTGGGGGAGG
DR20006	C-----	TCGAG---TCTGGAGGGAGG
DR21006	C-----	TCGAG---TCTGGGGGAGG
DR09006	C-----AGGTGA-----	AACTGCTCGAG---TCTGGGGGAGG
DR17006	C-----	TCGAG---TCTGGGGGAGG
DR13006	C-----	TCGAG---TCAGGGGGAGG
DR02006	CTCGAGTCAGGTGTCCGGTCTGATGTGCAGCTGGTGGCGTCTGGGGGAGG	

DR11006	ATCGGTGCAGGGCTGGAGGGTCTCTGAGACTCTC--GTGCG-CAGCCTCTG
DR27006	CTCGGTGCAGGGCTGGAGGGTCTCTGAGACTCTCCTGTGCATCTTCTCTA
DR13006	CTCGGTGCAGACTGGAGGATCTCTGAGACTCTCCTGTGCAGT--C-TCTG
DR11006	CTCGGTGCAGGGCTGGAGGGTCTCTGAGACTCTCCTGTAAATGT--C-TCTG
DR24006	CTCGGTGCAGGGCTGGAGGGTCTCTGAGACTCTCCTGTAAATGT--C-TCTG
DR16006	CTCGGCGCAGGGCTGGAGGATCTCTGAGACTCTCCTGTGCAGC--CCACGG
DR19006	CTCGGTTCAAGGCTGGAGGGTCCCTTAGACTCTCCTGTGCAGC--C-TCTG
DR17006	CTCGGTGCAGGGTGGAGGGTCTCTGAGACTCTCCTGTGCAA--TCTCTG
DR16006	CTCGGTGCAGGGCTGGAGGGTCTCTGAGACTCTCCTGTACAG---GCTCTG
DR20006	CTCGGTACAGGTTGGAGGGTCTCTGAGACTCTCCTGTGTAG---CCTCTA
DR25006	CTCGGTACAAACTGGAGGGTCTCTGAGACTCTCTTGCG---AAATCTCTG
DR20006	CTCGGTGCAGGGCTGGAGGGTCTCTGAGACTCTCCTGTG---TAGCCTCTG
DR21006	CTCGGTGCAGGGTGGAGGGTCTCTGAAACTCTCCTGTAAAAT---CTCTG
DR09006	CTCGGTGCAGGGCTGGGGGGTCTCTGACACTCTCTTGCG---TATAACAC--
DR17006	CTCGGTCCAACCTGGAGGATCTCTGACACTCTCCTGTACAGTT---TCTG
DR13006	CTCGGTGGAGGGCTGGAGGGTCTCTGAGACTCTCCTGTACAG---CCTCTG
DR02006	CTCGGTGCAGGGCTGGAGGGTCTCTGAGACTCTCCTGTACAG---CCTCTG

DR01006	GA--TACAGTAATT---GTCCCCCTCACTTG-GAGCTGGTATGCCAGTTT
DR27006	AA--TATATGCCCTT---GCACCTACGACAT-GACCTGGTACCGCCAGGCT
DR03006	GA--TTCTCCTTTA---GTACCAGTTGTAT-GGCCTGGTTCCGCCAGGCT
DR11006	GC--TCTCCCAGTA---GTACTTATTGCCT-GGCCTGGTTCCGCCAGGCT
DR24006	GC--TCTCCCAGTA---GTACTTATTGCCT-GGCCTGGTTCCGCCAGGCT
DR16006	GA--TTCCGC-TCA---ATGGTTACTACAT-CGCCTGGTTCCGTACGGCT
DR19006	AC--TACACCATCA---CTGATTATTGCAT-GGCCTGGTTCCGCCAGGCT
DR07006	GA--TACACGTACG---GTAGCTTCTGTAT-GGCCTGGTTCCGCCAGGCT
DR16006	GA--TTCCCCCTATA---GTACCTTCTGTCT-GGGGTGGTTCCGCCAGGCT
DR20006	CT--CACACCGACA---GTAGCACCTGTAT-AGGCTGGTTCCGCCAGGCT
DR25006	GA--TTGACTTTG---ATGATTCTGACGT-GGGGTGGTACCGCCAGGCT
DR20006	GA--TTCAATTTCG---AAACTCTCGTAT-GGCCTGGTACCGCCAGACT
DR21006	GAGGTACCCAGATCGTGTCTAAATCTTGGCCTGGTTCCGCCAGGCT

DR09006 -----CAACGATACTGGGACCA-----TGGGATGGTTGGCAGGGCT
 DR17006 --GGGGCACCTACA---GTGACTACAGTATTGGA-TGGATCGGCCAGGGCT
 DR13006 G-----ATACGTTAT-CCT---CTATGGCCTGGTTCCGCCAGGGTT
 DR02006 GAGA----CAGTTTCAGTAGATT--TGCATGCTTGTTCCGCCAGGGCT

DR01006 CCAGGAACGGAGCGCGAGTTCGTCCTCAGTATGGATCCGGATGGAAATAC
 DR27006 CCAGGAAGGAGCGCGAATTGTCCTCAAGTATAATATTGATGGTAAGAC
 DR03006 TCAGGAAAGCAGCGTGAGGGGGTCGAGGCCATTAATAGTGGCGGTGGTAG
 DR11006 CCAGGGAGGGAGCGTGAGGGGGTCACAGCGATTAA-----CACTGATGG
 DR24006 CCAGGGAGGGAGCGTGAGGGGGTCACAGCGATTAA-----CACTGATGG
 DR16006 CCTGGGAAGGGCGTGAGGGGGTCGAACAATTAAATGGTGGTCG-----
 DR19006 CCAGGGAGGAGCGTGAAATTGGTCGAGCGATTCAAGTTGTCGTAGTGA
 DR07006 CCAGGCAAGAACGTGAGGGGATCGCAACTATTCTTAATGGTGGTACTAA
 DR16006 CCAGGGAGGAGCGTGAGGGGGTCGCGGGTATTAATAGTGCAGGAGGTAA
 DR20006 CCAGGGAGGAGCGCGAGGGGGTCGCAAGTATAATTTGGTGTGGTGG
 DR25006 CCAGGGCATGAGTGCAAATTGGTCTCAGGTATTCTGAGTGATGGTACT-C
 DR20006 CCAGGAAATGTGTGTGAGTTGGTCTCAAGTATTACAGTGATGG-----
 DR21006 CCAGAGAAGGAGCGCGAGGGGATCGCAGTTCTGACTAAGGATGGTAA
 DR09006 CCAGGGAAAGAGTGCIAAAGGGTCGCGCATATTACGCCGTGGTATGA-
 DR17006 CCAGGGAGGACCGTGAAGTAGTGCAGCCGCTAATACGGT-----
 DR13006 CCAGGGCAGGAGCGCGAGGGGGTCGCGTTGTTCAAACGG-----
 DR02006 CCAGGGAGGAGTGCAGTTGGTCTCAAGCATTCAAAGTAATGGAAGGAC

DR01006 CAAGTACA-----CATACTCCGTGAAGGGCCGCTTCACC
 DR27006 AACATACG-----CAGACTCCGTGAAGGGCCGATTCA
 DR03006 GACATACTA-CAACACATATGTCGCCGAGTCCGTGAAGGGCCGATTGCC
 DR11006 CAGTATCAT-ATACGCA-----GCCGACTCCGTGAAGGGCCGATTCA
 DR24006 CAGTGTCA-ATACGCA-----GCCGACTCCGTGAAGGGCCGATTCA
 DR16006 CGA-CGTCACATACTACGCCGACTCCGTGACGGGCCGATTAC
 DR19006 TACT--CGC-C-TCACAGACTACGCCGACTCCGTGAAGGGACGATTCA
 DR07006 -----CACATACTATGCCGACTCGGTGAAGGGCCGATTCA
 DR16006 -----TACTTACTATGCCGACGCCGTGAAGGGCCGATTCA
 DR20006 -----TACGAATTATCGCGACTCCGTGAAGGGCCGATTCA
 DR25006 CATATACAAAGAGTGGAGACTATGCTGAGTCTGTGAGGGGCCGGTTACC
 DR20006 CA-AAACATACTACGTCGACC--GCA-----TGAAGGGCCGATTCA
 DR21006 GA-----CATTCTATGCCGACTCCGTGAAGGGCCGATTCA
 DR09006 -----CCTTCATTGATGAACCCGTGAAGGGGCCGATTCA
 DR17006 -----CGACTAGTAAATTCTACGTCGACTTGTGAAGGGCCGATTCA
 DR13006 --CTGACAAT-AGTGCATTATATGGCGACTCCGTGAAGGGCCGATTCA
 DR02006 AACTGA-----GGCCGATTCCGTGCAAGGCCGATTCA

DR01006 ATGTCCGAGGCAGCACCGAGTACACAGTATTCTGAAATGGACAAATCT
 DR27006 ATCTCCAAGACAGCGCCAGAACACCGGTATCTGAGATGAACAGCCT
 DR03006 ATCTCCAAGACACGCCAGAACACCGGTATCTGATATGAACAACCT
 DR11006 ATCTCCAAGACACCGCCAGAACACCGGTACATCTCAGATGAACAACCT
 DR24006 ATCTCCAAGACACCGCCAGAACACCGGTATATCTCAGATGAACAACCT
 DR16006 ATCTCCGAGACAGCCCCAGAACACCGGTATCTGAGATGAACAGCCT
 DR19006 ATCTCCAAGGCACACCAAGAACACAGTGAATCTGAAATGAACAGCCT
 DR07006 ATCTCCAAGACACGCCAGAACACCGGTATCTGCTAATGAACAACCT
 DR16006 ATCTCCAAGGGAAATGCCAGAACACCGGTATCTGAAATGGATAACTT
 DR20006 ATCTCCAACCTAACGCCAGAACACAGTGTATCTGAAATGAACAGCCT
 DR25006 ATCTCCAGAGACACGCCAGAACACATGATATACCTTCAAATGAACAGCCT
 DR20006 ATTCTAGAGAGAATGCCAGAACACATTGTATCTACAACTGAGGGCCT
 DR21006 ATCTTCTTAGATAATGACAAGACCACTTCTCTTACAACATTGATCGACT
 DR09006 ATCTCCGAGACACGCCAGAACACGGTGTCTTGCAGATGAATAGTCT

DR17006 ATTTGCCAAGACAAAGCCAAAGAATACGGTATATCTGAAATGAGCTTGT
 DR13006 ATCTGCCACGACACGGCAAGAACACGCTGTATCTGAAATGCGCAACGCT
 DR02006 ATCTCCGAGACAAATTCCAGGAAACACAGTGTATCTGAAATGAAACAGCT

DR01006 GAAACCTGAGGACACGGCGATGTATTACTGTAAAAC-A---GCCCTAC--
 DR27006 GAAACCTGAGGACACGGCGATGTATTACTGTAAAAT-A---GA---TTC--
 DR03006 AACCCCTGAAGACACGGCTACGTATTACTGTGCGGGCGG---TCCCAGCCC
 DR11006 GCAACCTGAGGATAACGGCCACCTATTACTGCGCGGCACAA---GACTGACGG
 DR24006 GCAACCTGAGGATAACGGCCACCTATTACTGCGCGGCACAA---GACTGACGG
 DR16006 GAAACCTGAGGACACGGCCATCTACTCTGTGCGAGCAG---G----CTC
 DR19006 GACACCTGAGGACACGGCCATCTACAGTTGTGCGGCACAA---C----CAG
 DR07006 GAAACCTGAAGACACGGGCACCTATTACTGTGCTG-CACAA-GAACTAAGT
 DR16006 GAAACCTGAGGACACGGCCATCTATTACTGCGCGG-CG---GATAGTCCA
 DR20006 GAAACCTGAGGACAGGCCATGTACTACTGTGCAATCA---CTGAAATTG
 DR25006 GAAACCTGAGGACACGGCCATGTATTACTGCGCGTAGATGGTTGGACCC
 DR20006 CAAACCTGAGGACACGGCCATGTATTACTGTGCG-----CC
 DR21006 GAACCCGGAGGACACTGCGACTACTACTGCGCTGAAATCAATTAGC--
 DR09006 GAGGCCTGAGGACACGGCCGTATTACTGTGCGGCAGATTG-----
 DR17006 GAAACCTGAGGACACGGCCATCTATTACTGTGCGGCAG---CGGACCC
 DR13006 GCAACCTGACGACACTGGCGTGTACTACTGTGCGGCC---CAA
 DR02006 GAAACCCGAGGACACGGCCGTATTACTGTGGGGCAGT-----

DR01006 -----A-AC---CTGGGGGTTATTGTGGGT-----
 DR27006 -----GTAC---CCGTGCCATCTCCTTGATG-----
 DR03006 ACTTGGGACCT-----GGCG-CCATT-----CTTGATTG
 DR11006 AGATGGGGGCTTGTGATGCGAGATGGGCACCTTAGC---GACAAGGAC-G
 DR24006 AGATGGGGGCTTGTGATGCGAGATGGGCACCTTAGC---GACAAGGAC-G
 DR16006 GCGTTTTT-CTAGTCCCTGTTGGGAGCACTTC-TAGAC---TCGAAAGTAG
 DR19006 TAGTTTTTACTGGTACT-----GCAC-----C---ACG-----G
 DR17006 GGTGGTAGTTGTGAATTGC---CTTTGC-----TATTGACTA-----
 DR16006 TGTTACATGCCGACTATGC---CCGCTCCCCGATACGAGACAGTTTGG
 DR20006 AGTGGTATGGGTGCAATT-----AAGGACTACTTTACT---C-----G
 DR25006 GGAAGGAAG---GGGAATGGGTTAC---CCTGGTCGGTCCAATGTGAA
 DR09006 GGTTGAA-----TATC---CTATTGCAAGAC---ATGTGTT
 DR21006 ---TGGTGGCTGGTATT-----TGGACCGAATTACTGG-CTCTCTGTG
 DR09006 ---GAAATACTGGA---CTTGTGGTGC---CCAGA-CTGG-----AG
 DR17006 AAGTATATATTATAGTATC---CTCCNNAT-----
 DR13006 AAGAAGGATCGTA---CTAGATGGGC-----CGAGCCT-----
 DR02006 -----CTCCCTAA---TGGACCGAATTTC

DR01006 --TGGGTANTGCCCTGGGGCCAGGGGACCCAGGTACCCGTCTCCTCACT
 DR27006 --T-----CTGGGGCCAGGGGACCCAGGTACCCGTCTCCTCACT
 DR03006 AAAAAGTATAAGTACTGGGGCCAGGGGACCCAGGTACCCGTCTCCTCACT
 DR11006 TTTGCGTATAACTACTGGGGCCGGGGGACCCAGGTACCCGTCTCCTCACT
 DR24006 TTTGCGTATAACTACTGGGGCCGGGGGACCCAGGTACCCGTCTCCTCACT
 DR16006 CGA-CT-ATAACTATTGGGGCCAGGGGATCCAGGTACCCGTACCCGTACT
 DR19006 CGC-CTTATAACGTCTGGGTCAAGGGGACCCAGGTACCCGTCTCCTCACT
 DR07006 CTGGG-----GCCAGGGCACCCAGGTACCCGTCTCCTCACT
 DR16006 CTGGGATGATTT-----GGCCAGGGGACCCAGGTACCCGTCTCCTCACT
 DR20006 CTGGG-----GCCAGGGGACCCAGGTACCCGTCTCCTCACT
 DR25006 GATGGTTATAACTATTGGGGCCAGGGGACCCAGGTACCCGTCTCCTCAC
 DR20006 CGAGAT---ACG---GCGACCCGGGGACCCAGGTACCCGTCTCCTCAC
 DR21006 GGTGCATATGCCATCTGGGGCCAGGGGACCCAGGTACCCGTCTCCTCAC
 DR09006 GATACTTCGGACAG-TGGGTCAGGGGCCAGGGGACCCAGGTACCCGTCTCCTCACT
 DR17006 --TGAGTATAAGTACTGGGGCCAGGGGACCCAGGTACCCGTCTCCTCACT

DR13006	CGAGAATGGAAACAACTGGGGCCAGGGGACCCAGGTACCGTCTCCCTCA--
DR02006	CCAACATGGG--TCCCCGGGCCAGGAACCCAGGTACCGTCTCCCT----
DR01006	AG----TTACCCGTACGACGTTCCGGACTACGGTTCTTAATAGAATT
DR27006	AG----TTACCCGTACGAGGTTCCGGACTACGGTTCTTAATAGAATT
DR03006	AGCTAGTTACCCGTACGACGTTCCGGACTACGGTTCTTAATAGAATT
DR11006	AG----TTACCCGTACGACGTTCCGGACTACGGTTCTTAATAGAATT
DR24006	AGCTAGTTACCCGTACGACGTTCCGGACTACGGTTCTTAATAGAATT
DR16006	----AGTTACCCGTACGACGTTCCGGACTACGGTTCTTAATAGAATT
DR19006	----AGTTACCCGTACGACGTTCCGGACTACGGTTCTTAATAGAATT
DR07006	----AGTTACCCGTACGACGTTCCGGACTACGGTTCTTAATAGAATT
DR16006	----AGTTACCCGTACGACGTTCCGGACTACGGTTCTTAATAGAATT
DR20006	----AGTTACCCGTACGACGTTCCGGACTACGGTTCTTAATAGAATT
DR25006	---TAGTTACCCGTACGACGTTCCGGACTACGGTTCTTAATAGAATT
DR20006	---TAGTTACCCGTACGACGAACCGGACTACGGTTCTTAATAGAATT
DR21006	---TAGTTACCCGTACGACGTTCCGGACTACGGTTCTTAATAGAATT
DR09006	AGCTAGTTACCCGTACGACGTTCCGGACTACGGTTCTTAATAGAATT
DR17006	-----
DR13006	-----
DR12006	-----TA

FIGURE 7(4)

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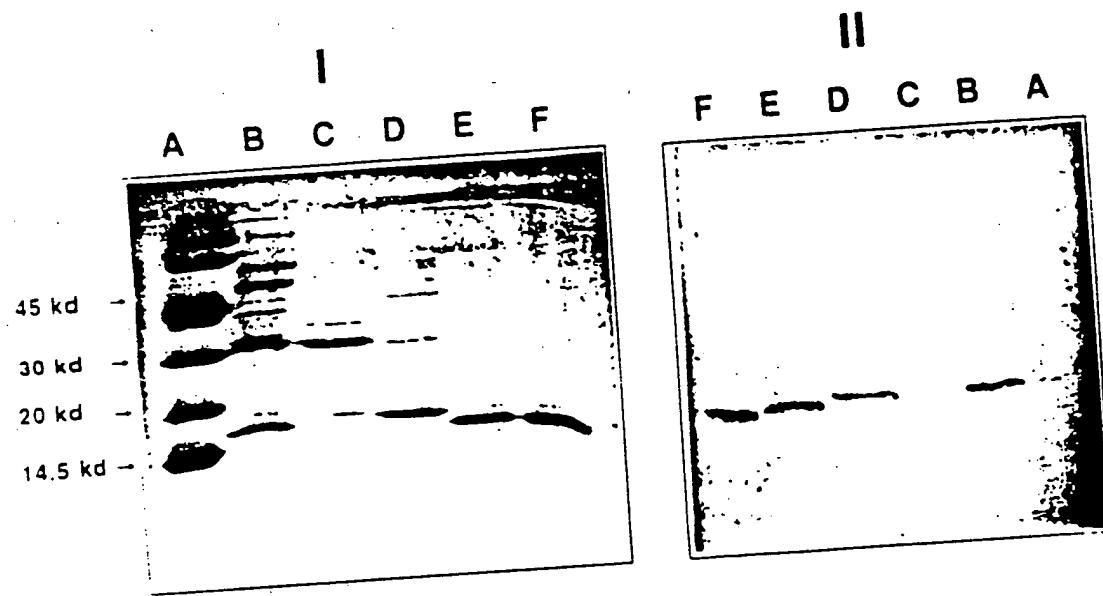
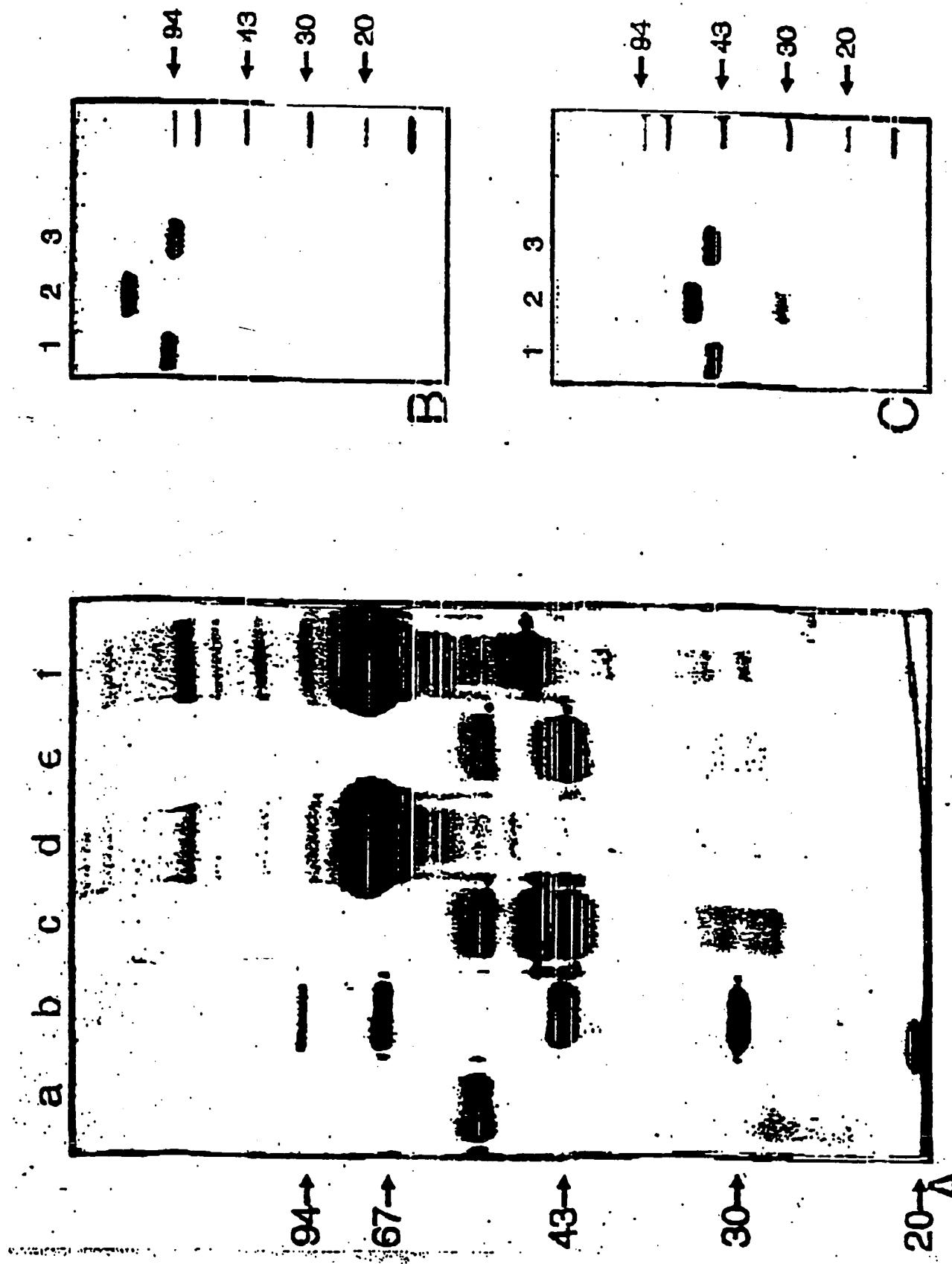
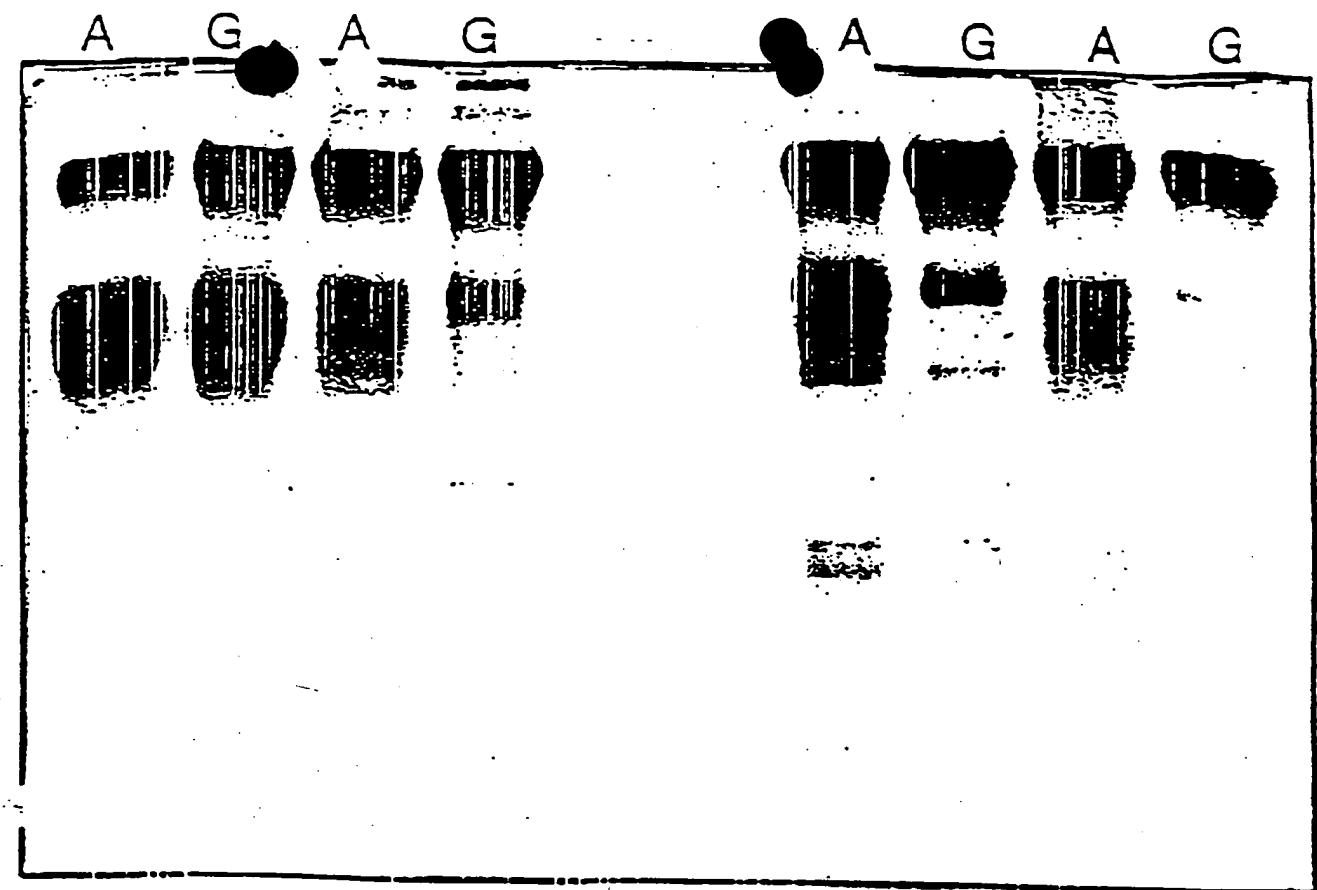


FIGURE 8

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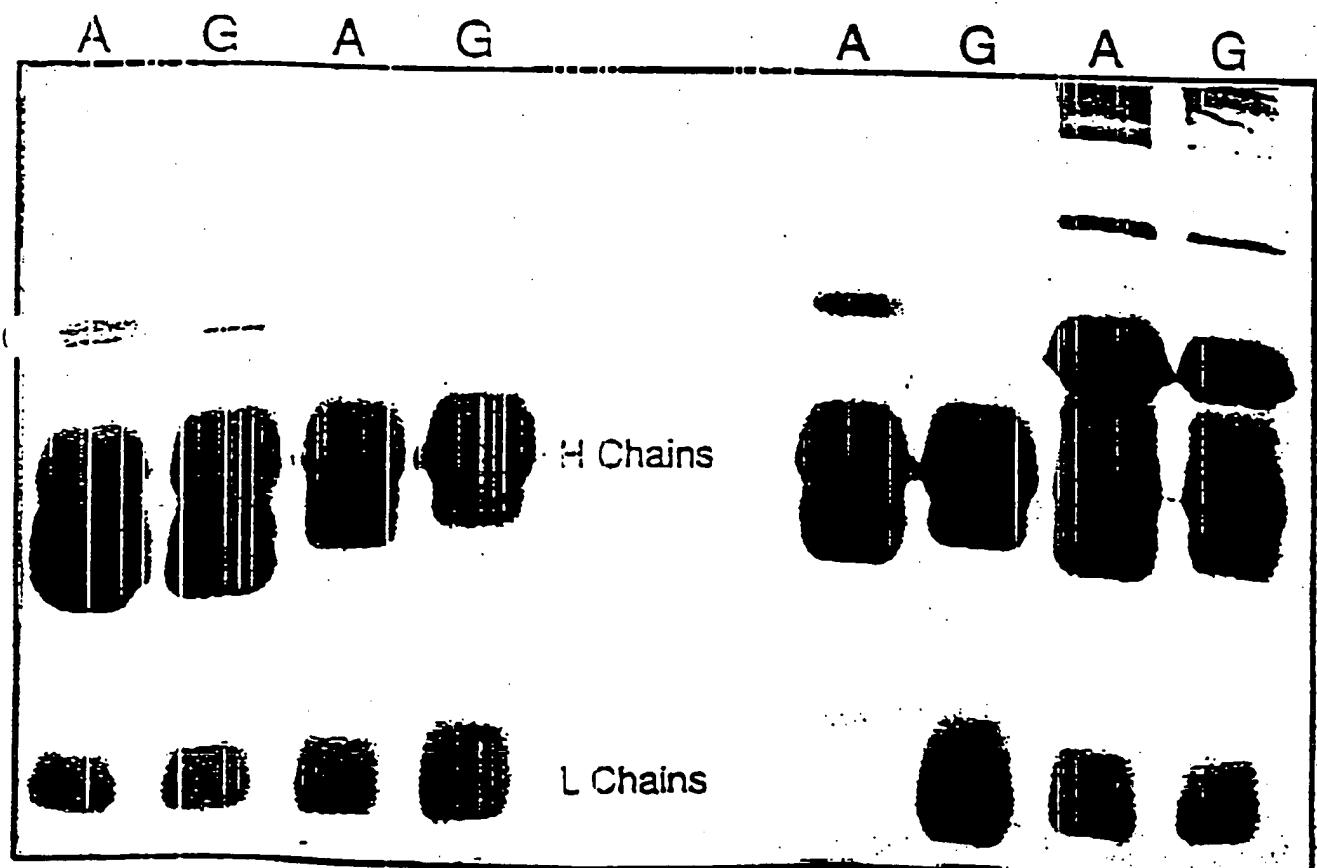
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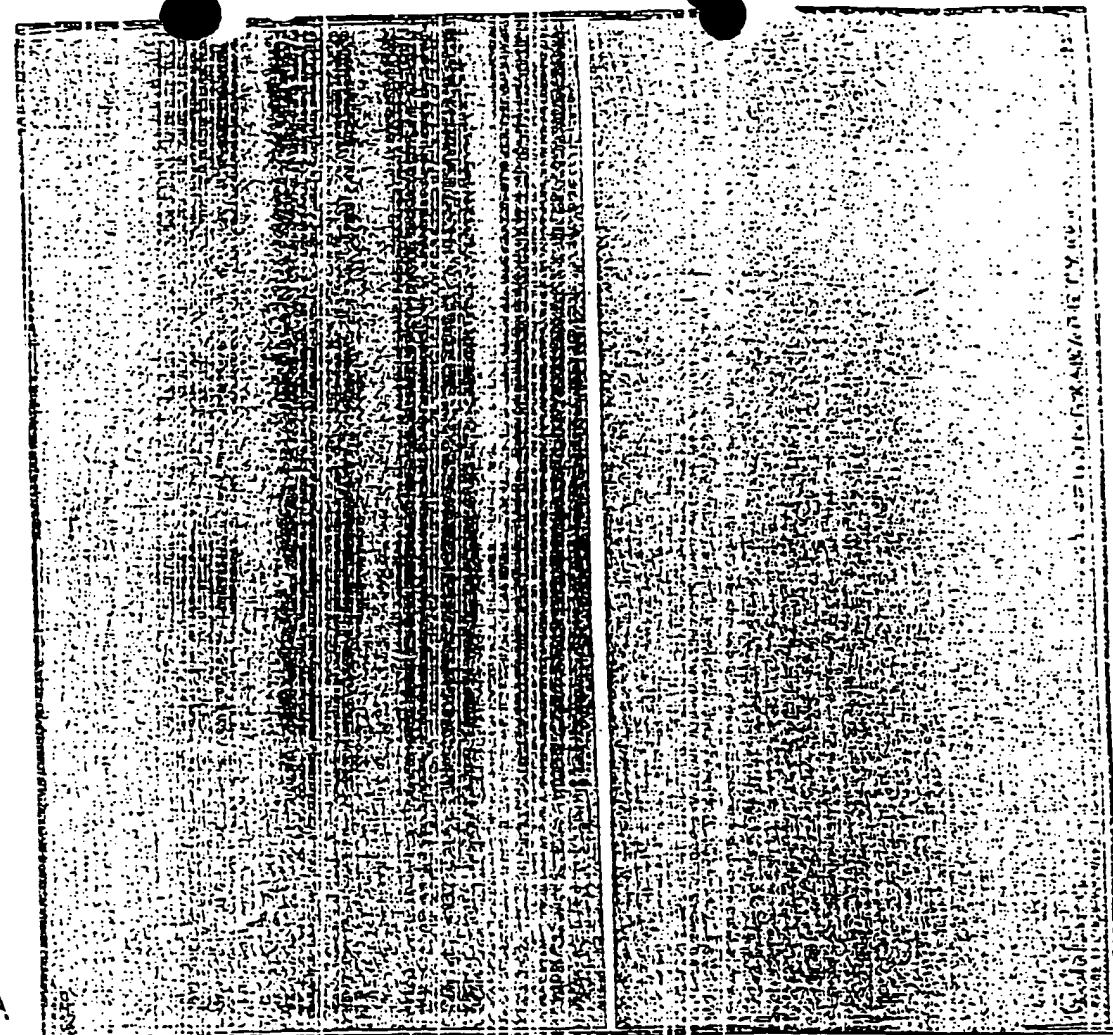


C. bactrianus *L. vicugna*

L. glama *L. pacos*



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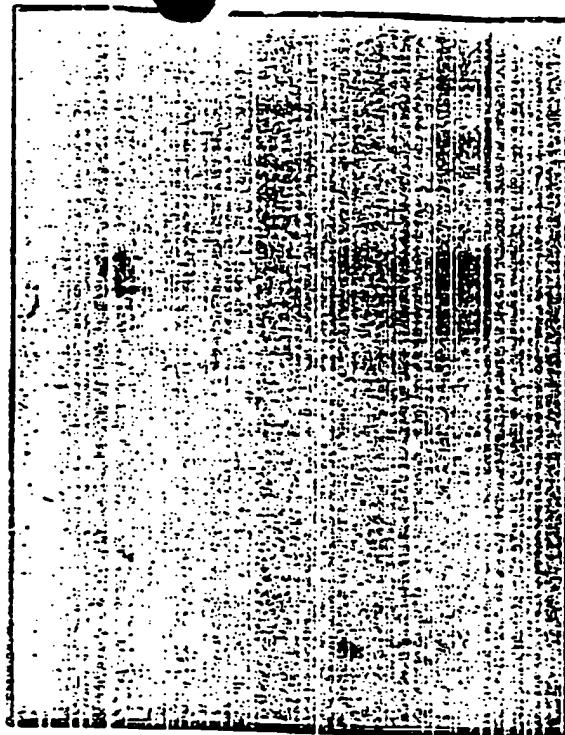


Prot. A	Ig1	Ig2	Ig3	Tct.Ser	Ig1	Ig2	Ig3	Tot.Ser	
Control	T. evansi infected				Healthy				
Units/5ul	65	1258	1214	2700	2978	147	157	160	107

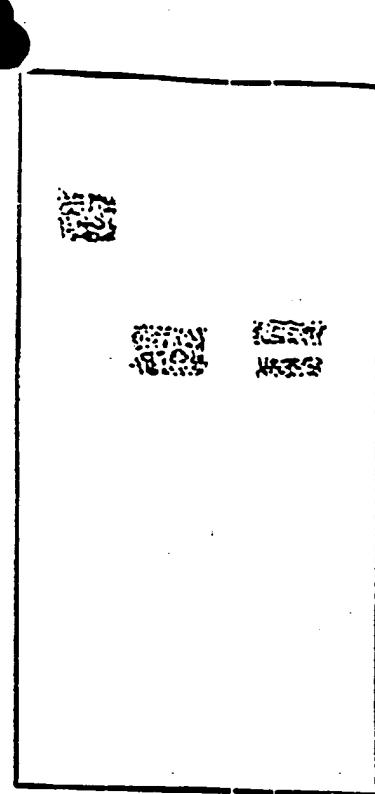
figure 3 (1)

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3 B



Ig1 Ig2 Ig3 Ig1 Ig2 Ig3
Healthy *T. evansi* infected



Ig1 Ig2 Ig3
Ponceau Red

figure 3 (2)

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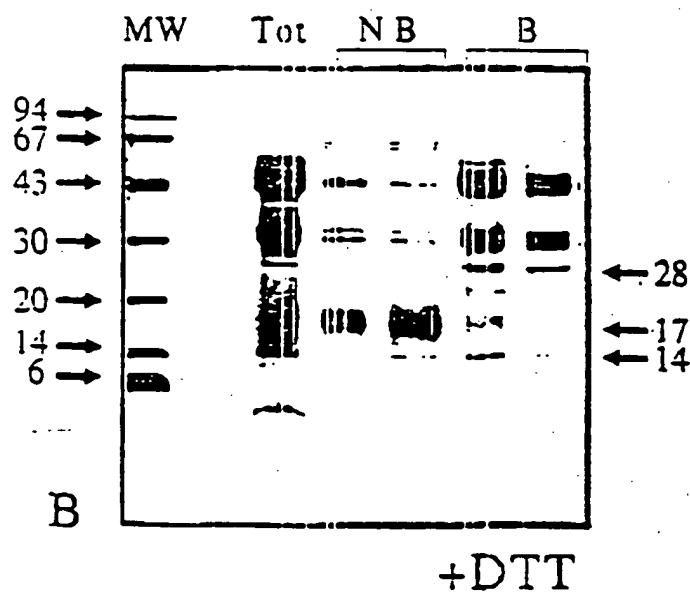
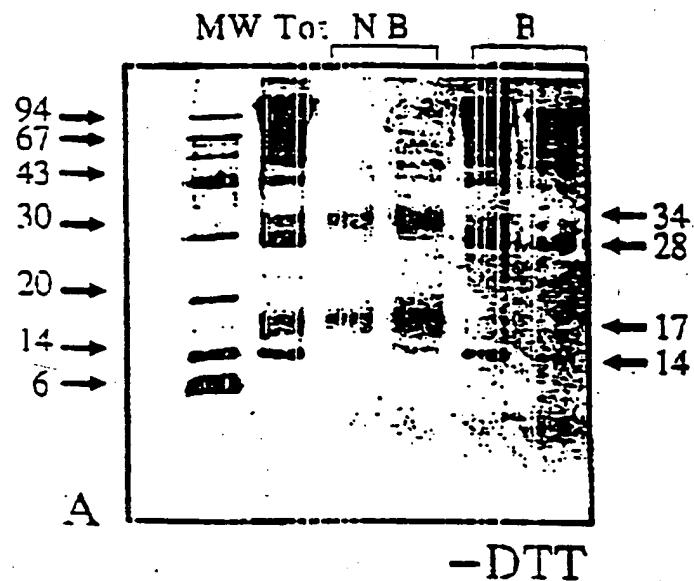


Fig 4 Analysis of IgG₃Papain Fragments by SDS - PAGE

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